



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/502,431

DATE: 07/30/2004

TIME: 16:22:00

Input Set : A:\64141-02.ST25.txt

Output Set: N:\CRF4\07302004\J502431.raw

3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS
 4 REPRESENTED BY THE
 5 Harris, Curtis C.
 6 Nagashima, Makoto
 7 Shiseki, Masayuki
 8 Pedoux, Remy
 10 <120> TITLE OF INVENTION: NEW TUMOR SUPPRESSOR GENE, p28ING5
 12 <130> FILE REFERENCE: 4239-64141-02
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/502,431
 C--> 14 <141> CURRENT FILING DATE: 2004-07-22
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/02174
 15 <151> PRIOR FILING DATE: 2003-01-23
 17 <150> PRIOR APPLICATION NUMBER: 60/351,504
 18 <151> PRIOR FILING DATE: 2002-01-23
 20 <160> NUMBER OF SEQ ID NOS: 2
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1068
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (3)..(725)
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 36 Met Ala Thr Ala Met Tyr Leu Glu His Tyr Leu Asp Ser Ile Glu
 37 1 5 10 15
 39 aac ctt ccc tgc gaa ctt cag agg aac ttc cag ctg atg cga gag ctg 95
 40 Asn Leu Pro Cys Glu Leu Gln Arg Asn Phe Gln Leu Met Arg Glu Leu
 41 20 25 30
 43 gac cag agg acg gaa gat aag aaa gca gag att gac atc ctg gct gca 143
 44 Asp Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu Ala Ala
 45 35 40 45
 47 gag tac atc tcc acg gtg aag acg ctg tct cca gac cag cgc gtg gag 191
 48 Glu Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg Val Glu
 49 50 55 60
 51 cgc ctg cag aag atc cag aac gcc tac agc aag tgc aag gaa tac agt 239
 52 Arg Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu Tyr Ser
 53 65 70 75
 55 gac gac aaa gtg cag ctg gcc atg cag acc tac gag atg gtg gat aaa 287
 56 Asp Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val Asp Lys
 57 80 85 90 95
 59 cac att cga agg ctt gat gca gac ctg gcg cgc ttt gaa gca gat ctg 335



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60 His Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala Asp Leu
61          100          105          110
63 aag gac aag atg gag ggc agt gat ttt gaa agc tcc gga ggg cga ggg      383
64 Lys Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly Arg Gly
65          115          120          125
67 tta aaa aaa ggc cgg ggt cag aaa gaa aaa aga ggg tcc cgg ggc cga      431
68 Leu Lys Lys Gly Arg Gly Gln Lys Glu Lys Arg Gly Ser Arg Gly Arg
69          130          135          140
71 ggc agg agg aca tca gag gaa gac aca cca aag aaa aag aag cac aaa      479
72 Gly Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys His Lys
73          145          150          155
75 gga ggg tct gag ttc act gac acc atc ctg tcc gtg cac ccc tct gat      527
76 Gly Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro Ser Asp
77 160          165          170          175
79 gtg ctg gac atg ccc gtg gac cca aac gaa ccc acg tac tgc ctg tgc      575
80 Val Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys
81          180          185          190
83 cac cag gtc tcc tat ggg gag atg att ggc tgt gac aat cca gac tgt      623
84 His Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro Asp Cys
85          195          200          205
87 cca att gag tgg ttt cac ttt gcc tgc gtg gac ctt acc acg aaa ccc      671
88 Pro Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr Lys Pro
89          210          215          220
91 aaa gga aaa tgg ttc tgt cca cgg tgt gtc cag gaa aag agg aag aag      719
92 Lys Gly Lys Trp Phe Cys Pro Arg Cys Val Gln Glu Lys Arg Lys Lys
93          225          230          235
95 aag tag gaggagctgt gtgcccggat ccgaggagca agttaatctg tcccttcatt      775
96 Lys
97 240
99 cgtgtcgcaa tatttccctt ccttttaaaa ctaccttggt cggttgatac ttagtaactc      835
101 cgtggccagt tgaagcgtg gatgtttcct agaacaagaa ccaccaaagc ctgttcgcac      895
103 agaagggcga ccttgcaggg actcgccgcc gcgacctcag tgtggctttt acaggactcc      955
105 ccccgagcat cagcagggac cccggcggac gtgggcgggc gcgcgtgagc tcgggctgcc      1015
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111 <211> LENGTH: 240
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
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121 Leu Pro Cys Glu Leu Gln Arg Asn Phe Gln Leu Met Arg Glu Leu Asp
122          20          25          30
125 Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu Ala Ala Glu
126          35          40          45
129 Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg Val Glu Arg
130          50          55          60
133 Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu Tyr Ser Asp
134 65          70          75          80

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137 Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val Asp Lys His
138           85                      90                      95
141 Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala Asp Leu Lys
142           100                      105                      110
145 Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly Arg Gly Leu
146           115                      120                      125
149 Lys Lys Gly Arg Gly Gln Lys Glu Lys Arg Gly Ser Arg Gly Arg Gly
150           130                      135                      140
153 Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys His Lys Gly
154 145           150                      155                      160
157 Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro Ser Asp Val
158           165                      170                      175
161 Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys His
162           180                      185                      190
165 Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro Asp Cys Pro
166           195                      200                      205
169 Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr Lys Pro Lys
170           210                      215                      220
173 Gly Lys Trp Phe Cys Pro Arg Cys Val Gln Glu Lys Arg Lys Lys Lys
174 225           230                      235                      240

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VERIFICATION SUMMARY

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Input Set : A:\64141-02.ST25.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date